# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: _____10/559, 825_____

Source: _____JFWP_____

Date Processed by STIC: _____12/16/2005_____

# *ENTERED*

RAW SEQUENCE LISTING                    DATE: 12/16/2005
PATENT APPLICATION:   US/10/559,825    TIME: 15:33:38

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12162005\J559825.raw**

```
 3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 4        REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 5        HUMAN SERVICES
 6        Schneerson, Rachel
 7        Leppla, Stephen H.
 8        Robbins, John B.
 9        Shiloach, Joseph
10        Kubler-Kielb, Joanna
11        Liu, Darrell
12        Majadly, Fathy
14 <120> TITLE OF INVENTION: GAMMA PGA CONJUGATES FOR ELICITING IMMUNE RESPONSES DIRECTED
15        AGAINST BACILLI
17 <130> FILE REFERENCE: 4239-68226-07
```
C--> `19 <140> CURRENT APPLICATION NUMBER: US/10/559,825`
C--> `19 <141> CURRENT FILING DATE: 2005-12-02`
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19 <150> PRIOR APPLICATION NUMBER: PCT/US2004/017736
20 <151> PRIOR FILING DATE: 2004-06-04
22 <150> PRIOR APPLICATION NUMBER: US 60/476,598
23 <151> PRIOR FILING DATE: 2003-06-05
25 <160> NUMBER OF SEQ ID NOS: 3
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 13
31 <212> TYPE: PRT
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Basic peptide derived from HIV-1 Tat protein.
37 <400> SEQUENCE: 1
39 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
40 1               5                   10
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 2295
45 <212> TYPE: DNA
46 <213> ORGANISM: Bacillus anthracis
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (1)..(2292)
53 <400> SEQUENCE: 2
54 atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata        48
55 Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile
56 1               5                   10                  15
58 tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa        96
59 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
```

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60           20                25                30
62 cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta     144
63 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
64           35                40                45
66 cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt     192
67 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
68           50                55                60
70 acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa     240
71 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
72 65                70                75                80
74 aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga     288
75 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
76           85                90                95
78 ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct     336
79 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
80           100               105               110
82 gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa     384
83 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
84           115               120               125
86 gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa     432
87 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
88           130               135               140
90 ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat     480
91 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
92 145               150               155               160
94 ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct     528
95 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
96           165               170               175
98 agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca     576
99 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
100          180               185               190
102 aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac    624
103 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
104          195               200               205
106 aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat    672
107 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
108          210               215               220
110 gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat    720
111 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
112 225               230               235               240
114 gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc    768
115 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
116          245               250               255
118 acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att    816
119 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
120          260               265               270
122 gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat    864
123 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
124          275               280               285
```

```
126 ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag        912
127 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
128     290             295                 300
130 gat caa tcc aca cag aat act gat agt caa acg aga aca ata agt aaa        960
131 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
132 305             310                 315                 320
134 aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca       1008
135 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
136             325                 330                 335
138 gaa gtg cat gcg tcg ttc ttt gat att ggt ggg agt gta tct gca gga      1056
139 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
140             340                 345                 350
142 ttt agt aat tcg aat tca agt acg gtc gca att gat cat tca cta tct      1104
143 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
144             355                 360                 365
146 cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct      1152
147 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
148     370                 375                 380
150 gat aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg      1200
151 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
152 385             390                 395                 400
154 gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa      1248
155 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
156             405                 410                 415
158 aat caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa      1296
159 Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
160             420                 425                 430
162 ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc      1344
163 Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile
164             435                 440                 445
166 gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat      1392
167 Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
168     450                 455                 460
170 tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat      1440
171 Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
172 465             470                 475                 480
174 acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga      1488
175 Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
176             485                 490                 495
178 aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg caa      1536
179 Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
180             500                 505                 510
182 att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta aat      1584
183 Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn
184             515                 520                 525
186 ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa      1632
187 Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
188     530                 535                 540
190 acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt      1680
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191 Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
192 545             550             555             560
194 gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata      1728
195 Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
196             565             570             575
198 acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag      1776
199 Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
200             580             585             590
202 aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat      1824
203 Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
204             595             600             605
206 aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt      1872
207 Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
208     610             615             620
210 ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta      1920
211 Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
212 625             630             635             640
214 gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta      1968
215 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
216             645             650             655
218 ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att      2016
219 Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
220             660             665             670
222 gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga      2064
223 Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
224             675             680             685
226 tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt      2112
227 Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
228     690             695             700
230 ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat      2160
231 Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
232 705             710             715             720
234 ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att      2208
235 Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
236             725             730             735
238 att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa      2256
239 Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
240             740             745             750
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243 Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
244             755             760
247 <210> SEQ ID NO: 3
248 <211> LENGTH: 764
249 <212> TYPE: PRT
250 <213> ORGANISM: Bacillus anthracis
252 <400> SEQUENCE: 3
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255 1               5               10              15
258 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys
```

```
259              20                25                30
262 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
263          35                40                45
266 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
267      50                55                60
270 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
271 65                70                75                80
274 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
275              85                90                95
278 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
279          100               105               110
282 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
283          115               120               125
286 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
287      130               135               140
290 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
291 145               150               155               160
294 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
295              165               170               175
298 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
299          180               185               190
302 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
303          195               200               205
306 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
307      210               215               220
310 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
311 225               230               235               240
314 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
315          245               250               255
318 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
319          260               265               270
322 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
323      275               280               285
326 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
327      290               295               300
330 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
331 305               310               315               320
334 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
335          325               330               335
338 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
339          340               345               350
342 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
343          355               360               365
346 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
347      370               375               380
350 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
351 385               390               395               400
354 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
355              405               410               415
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VERIFICATION SUMMARY                          DATE: 12/16/2005
PATENT APPLICATION:  US/10/559,825            TIME: 15:33:39

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12162005\J559825.raw**

L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date